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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235152-SC **Lot No.: C101109**

Species: ■Human □ Mouse □ Rat □ Monkey (Rh) □ Guinea Pig □ Porcine
□ Bovine □ Hamster □ Dog □ Monkey (Cy) □ Rabbit □ Plant

Tissue Type: □ Normal □ Adult □ Fetal ■ Tumor □Disease □ Cell line

Tissue Name: Lung

Donor Information:

Male: 60 year(s) old
Female: _____year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: diameter 5 cm

Location: Lung, Left Lower Lobe

Components:
1. **5 curls per package**
2. **Certificate of Analysis**

FOR IN VITRO RESEARCH USE ONLY **APPROVED BY:** _____

C101109

For CNV mutations, we utilize stringent criteria to confirm copy number variations -- using normal tissues as controls. We may have samples containing additional CNVs not listed here. Please inquire.

tissue type	Lot #	Strong Evidence compared with **GIAB** (NA12878)	Copy Number	STDev of Copy Number	P-value
Lung	C101109	NOTCH1	5.72	0.10	1.42E-03
		MYC	13.78	0.29	1.42E-03
		CDKN2A	5.63	0.08	5.74E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
ABL1	snp	chr9	1.34E+08	C	T	323.359	hom	12	1.00	NM_00731	missense_variant	
AKT1	snp	chr14	1.05E+08	G	C	65.8514	het	40	0.25	NM_00101	splice_region_variant&	
ALK	snp	chr2	29432625	C	A	7921.56	het	349	0.89	NM_00430	intron_vari	rs3738868
ALK	snp	chr2	29432776	T	C	899.255	het	52	0.58	NM_00430	intron_vari	rs3738867
ALK	snp	chr2	29443749	G	T	1617.92	hom	58	0.97	NM_00430	intron_vari	rs8015297(
ALK	snp	chr2	29445389	A	G	1049.95	het	77	0.49	NM_00430	synonymous_variant	
APC	snp	chr5	1.12E+08	G	A	4723.18	het	271	0.63	XM_00527	missense_variant	
ATM	snp	chr11	1.08E+08	C	T	245.318	het	17	0.76	NM_00005	missense_variant	
AURKA	snp	chr20	54945545	G	A	244.485	het	13	0.85	NM_00360	missense_variant	
BRAF	complex	chr7	1.4E+08	AAG	TAC	6881.12	hom	249	0.98	XM_00525	missense_variant	
BRAF	complex	chr7	1.4E+08	CTTGATA	TATCAAG	7084.6	hom	250	1.00	XM_00525	splice_acceptor_varian	
CCND1	snp	chr11	69460769	G	A	1567.36	het	74	0.81	NM_05305	intron_variant	
CDH1	snp	chr16	68771244	G	A	1110.6	het	46	0.91	NM_00436	5_prime_UTR_variant	
CDH1	snp	chr16	68849366	C	T	2130.07	hom	93	1.00	NM_00436	intron_variant	
CDH1	snp	chr16	68849484	G	T	181.822	het	131	0.25	NM_00436	stop_gaine	COSM2083
CDKN2A	snp	chr9	21965743	C	T	5520.86	het	381	0.51	NM_00119	downstream_gene_var	
CDKN2A	snp	chr9	21968198	CC	CG	46471.2	hom	1636	0.90	NM_00119	3_prime_UTR_variant	
CDKN2A	mnp	chr9	21968198	CC	TG	4561.93	hom	160	0.99	NM_00119	3_prime_UTR_variant	
CDKN2A	snp	chr9	21968199	C	G	360.199	hom	12	1.00	NM_00119	3_prime_U	rs11515&C

CSF1R	snp	chr5	1.49E+08	C	T	401.075	het	22	0.73	NM_00521	synonymous_variant	
DDR2	mnp	chr1	1.63E+08	GC	AT	185.785	het	366	0.12	XM_00524	intron_variant	
DDR2	snp	chr1	1.63E+08	T	C	6500.34	hom	204	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	549.992	hom	24	1.00	XM_00524	intron_vari	rs1355287
DDR2	snp	chr1	1.63E+08	C	T	2874.07	het	165	0.62	XM_00524	splice_region_variant&	
DDR2	snp	chr1	1.63E+08	C	A	2751.33	het	216	0.45	XM_00524	missense_variant	
DDR2	snp	chr1	1.63E+08	C	T	1482.82	het	341	0.21	XM_00524	3_prime_UTR_variant	
EGFR	snp	chr7	55242479	C	T	4398.45	het	497	0.33	NM_00522	missense_variant	
EGFR	snp	chr7	55242487	C	T	2337.13	het	502	0.22	NM_00522	missense_v	rs1219132
ERBB2	snp	chr17	37881162	A	T	1021	het	1066	0.13	NM_00444	stop_gained&splice_re	
ERBB2	snp	chr17	37881206	C	A	2588.17	hom	139	0.99	NM_00444	intron_variant	
ERBB2	snp	chr17	37881471	C	T	3688.26	het	375	0.35	NM_00444	intron_variant	
ERBB3	snp	chr12	56477694	A	T	4779.74	hom	172	0.99	NM_00198	splice_regi	rs2271194
ERBB4	snp	chr2	2.13E+08	A	T	1327.54	het	166	0.31	NM_00523	intron_vari	rs3512391
ERBB4	snp	chr2	2.13E+08	A	G	1326.92	het	366	0.19	NM_00523	synonymous_variant	
ESR1	snp	chr6	1.52E+08	G	A	3137.28	hom	112	0.97	XM_00526	synonymou	rs2228480
FGFR2	snp	chr10	1.23E+08	G	A	426.593	het	240	0.15	NM_02297	intron_variant	
FGFR3	snp	chr4	1803757	G	A	103.355	het	83	0.14	NM_00116	splice_region_variant&	
FGFR3	snp	chr4	1803779	C	T	568.173	het	107	0.24	NM_00116	intron_vari	rs3726566
FGFR3	snp	chr4	1805432	A	G	410.408	het	67	0.27	NM_00116	intron_vari	rs3714109
FGFR3	snp	chr4	1806238	C	T	1884.05	het	380	0.22	NM_00116	synonymous_variant	
FGFR3	snp	chr4	1808286	G	A	2655.91	hom	92	1.00	NM_00116	missense_variant	
FLT3	snp	chr13	28610183	A	G	2228.16	hom	71	1.00	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	1.39E+08	G	A	922.13	hom	51	1.00	NM_02306	missense_v	COSM1419
H3F3A	complex	chr1	2.26E+08	CAA	AAT	9690.91	hom	366	0.97	NM_00210	stop_gained	
HRAS	snp	chr11	533690	A	G	324.389	het	106	0.21	NM_00534	intron_variant	
IDH1	snp	chr2	2.09E+08	G	A	1458.28	het	169	0.33	XM_00524	synonymous_variant	
JAK2	snp	chr9	5068984	G	A	285.319	hom	10	1.00	NM_00497	intron_variant	
KIT	snp	chr4	55599336	C	T	2339.6	het	101	0.91	XM_00526	missense_v	COSM1056
KIT	snp	chr4	55599382	C	T	2504.94	hom	89	1.00	XM_00526	intron_variant	
MAP2K1	snp	chr15	66727597	G	C	4384.64	het	180	0.86	NM_00275	intron_vari	rs1694992
MET	snp	chr7	1.16E+08	T	C	598.881	het	90	0.28	XM_00525	missense_variant	
MET	snp	chr7	1.16E+08	C	T	4178.89	hom	146	1.00	XM_00525	missense_v	rs2016283
MET	snp	chr7	1.16E+08	G	A	2205.38	hom	76	1.00	XM_00525	missense_variant	

MET	snp	chr7	1.16E+08	C	T	1390.2	het	65	0.85	XM_00525	intron_variant	
MYC	snp	chr8	1.29E+08	TCC	TCA	865.066	het	556	0.14	NM_00246	intron_variant	
MYC	snp	chr8	1.29E+08	C	T	4568.37	het	284	0.56	NM_00246	missense_variant	
MYCN	snp	chr2	16089671	T	C	1860.95	het	181	0.37	NM_00537	downstream_gene_va	
NOTCH1	snp	chr9	1.39E+08	G	A	522.356	het	77	0.29	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	401.369	het	402	0.13	NM_01761	synonymou	COSM7531
NPM1	del,del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	601.461	het	76	0.33	NM_00252	splice_region_variant&	
NRAS	snp	chr1	1.15E+08	T	A	557.704	hom	24	1.00	NM_00252	missense_variant	
NRAS	snp	chr1	1.15E+08	G	A	11.8452	het	167	0.11	NM_00252	missense_variant	
PDGFRA	snp	chr4	55161254	C	T	2946.67	hom	100	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161332	A	G	75.5343	het	84	0.14	NM_00620	missense_variant	
PDGFRA	snp	chr4	55161517	A	G	336.963	hom	11	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	G	T	202.168	het	44	0.34	NM_00621	missense_v	rs2019466
PTEN	complex	chr10	89720957	AAGA	GAGT	314.197	hom	22	1.00	NM_00031	intron_variant	
RB1	snp	chr13	48941654	G	A	4596.36	hom	170	0.97	NM_00032	missense_v	CM071073
RB1	del	chr13	49037778	TTTGA	TA	394.221	hom	14	1.00	NM_00032	intron_variant&feature	
RB1	complex	chr13	49037784	GCTA	CCTCAAA	399.664	hom	14	1.00	NM_00032	intron_variant&feature	
RET	mnp	chr10	43610189	GGG	TCT	461.414	hom	17	1.00	NM_02097	splice_region_variant&	
RET	mnp	chr10	43610199	GGG	CCC	565.454	hom	20	1.00	NM_02097	intron_variant	
SMAD4	snp	chr18	48593496	G	A	11341.8	hom	393	1.00	NM_00535	missense_v	COSM1389
SMO	snp	chr7	1.29E+08	G	C	773.705	hom	31	1.00	NM_00563	intron_vari	rs2075777
STK11	snp	chr19	1207238	G	T	6669.92	hom	236	0.99	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1218523	G	T	1046.12	hom	37	1.00	XM_00525	intron_vari	rs2075604
STK11	ins	chr19	1219443	GCGGGGG	GCGGGGG	318.975	hom	14	1.00	XM_00525	intron_variant&feature	
STK11	snp	chr19	1220289	G	A	79.9533	het	376	0.11	XM_00525	intron_variant	
STK11	snp	chr19	1220315	G	A	328.042	het	350	0.13	XM_00525	intron_variant	
STK11	snp	chr19	1220321	T	C	8695.61	hom	276	1.00	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1221208	G	A	1866.95	het	284	0.27	XM_00525	splice_region_variant&	
STK11	snp	chr19	1221965	CC	CT	24418.9	het	1146	0.82	XM_00525	missense_variant	
TERT	snp	chr5	1295305	G	T	417.128	het	159	0.18	NM_19825	upstream_gene_variar	
TERT	snp	chr5	1295349	A	G	6508.65	het	1200	0.22	NM_19825	upstream_	rs2853669
TP53	snp	chr17	7579472	G	C	2276.94	hom	79	0.99	NM_00054	missense_v	rs1042522
VHL	snp	chr3	10183642	G	A	5135.87	het	423	0.43	NM_00055	synonymous_variant	
VHL	snp	chr3	10188188	G	A	389.363	het	115	0.19	NM_00055	intron_vari	rs1400648

VHL	snp	chr3	10188293	C	T	1211.24	hom	46	0.96	NM_00055	missense_v	COSM1764